IN THE SPECIFICATION:

Please amend the paragraph beginning on page 7, line 6 as follows:

Figure 2 shows an alignment of Human Nod2 and Related Proteins. Figure ~~1~~2A shows an alignment of CARDs of Nod2 (SEQ ID NOs:5 and 6), Nod1 (GeneBank accession number AF113925; SEQ ID NO:20), RICK (AF027706; SEQ ID NO:21), ARC (AF043244; SEQ ID NO:22), RAIDD (U79115; SEQ ID NO:23), Caspase-2 (U13021; SEQ ID NO:24), Ced-3 (L29052; SEQ ID NO:25), Ced-4 (X69016; SEQ ID NO:26), Caspase-9 (U56390; SEQ ID NO:27), Apaf-I (AF013263; SEQ ID NO:28) and c-IAP-1 (L49431; SEQ ID NO:29). Hydrophobic residues are shown in reverse highlighting. Negatively and positively charged residues are highlighted in light and dark gray, respectively. Proline and glycine residues ((αβ breaker) are bolded. The putative (αhelices, Hl to H5, are shown according to the three dimensional structure of the CARD of RAIDD (Chou *et al.*, Cell, 94:171 [1998]). Figure 2B shows an alignment of NBDs of Nod2 (SEQ ID NO:7), Nodl (SEQ ID NO:30), Apaf-I (SEQ ID NO:31) and Ced-4 (SEQ ID NO:32). The residues identical and similar to those of Nod2 are shown by reverse and dark highlighting, respectively. The consensus sequence of the P-loop (Walker A box) and the Mg^{2+} binding site (Walker B box) are indicated by boxes. The residues identical and similar to those of Nod2 are shown by reverse and dark highlighting, respectively. Figure 2C shows an alignment of LRRs of Nod2 (SEQ ID NOs: 8-17). The conserved positions with leucine and other hydrophobic residues are indicated by dark and light gray highlighting, respectively. The putative (αhelix and βsheet are shown according to the three dimensional structure of the ribonuclease inhibitor (Kobe and Deisenhofer, Curr. Opin. Struct Biol., 5:409-416 [1995]).